

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/022,390A

Source: 1Fw/6

Date Processed by STIC: 1/10/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/10/2006

PATENT APPLICATION: US/10/022,390A

TIME: 14:30:41

Input Set : E:\912SEQ.002.txt

Output Set: N:\CRF4\01102006\J022390A.raw

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3 <110> APPLICANT: Vega, Manuel
4      Drittanti, Lila
5      Flaux, Marjorie
7 <120> TITLE OF INVENTION: MUTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES
9 <130> FILE REFERENCE: 37851-912
11 <140> CURRENT APPLICATION NUMBER: 10/022,390A
12 <141> CURRENT FILING DATE: 2001-12-17
14 <150> PRIOR APPLICATION NUMBER: 60/315,382
15 <151> PRIOR FILING DATE: 2001-08-27
18 <160> NUMBER OF SEQ ID NOS: 749
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 621
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Mutant rep protein: rep78 4 GCT
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32 1          5          10          15
33 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
34          20          25          30
35 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
36          35          40          45
37 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
38          50          55          60
39 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
40 65          70          75          80
41 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
42          85          90          95
43 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
44          100         105         110
45 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
46          115         120         125
47 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
48          130         135         140
49 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
50 145         150         155         160
51 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
52          165         170         175
53 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
54          180         185         190
55 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

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56		195		200		205										
57	Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
58		210					215					220				
59	Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
60	225					230					235				240	
61	Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
62					245					250					255	
63	Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
64				260					265					270		
65	Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
66			275					280					285			
67	Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
68		290					295					300				
69	Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
70	305					310					315				320	
71	Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
72					325					330					335	
73	Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
74				340					345					350		
75	Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
76			355					360					365			
77	Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
78		370					375				380					
79	Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
80	385					390					395				400	
81	Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
82				405						410					415	
83	Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
84				420					425					430		
85	Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
86			435					440					445			
87	Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
88		450					455					460				
89	Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
90	465					470					475				480	
91	Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
92				485						490					495	
93	Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
94				500					505					510		
95	Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
96			515					520					525			
97	Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
98		530					535					540				
99	Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
100	545					550					555				560	
101	Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
102					565					570					575	
103	Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
104				580					585					590		

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Input Set : E:\912SEQ.002.txt

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105 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
106           595                      600                      605
107 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
108           610                      615                      620
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 536
112 <212> TYPE: PRT
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Mutant rep protein: rep68 4 GCT
118 <400> SEQUENCE: 2
119 Thr Ala Gly Ala Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
120 1           5           10           15
121 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
122           20           25           30
123 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
124           35           40           45
125 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
126           50           55           60
127 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
128 65           70           75           80
129 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
130           85           90           95
131 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
132           100          105          110
133 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
134           115          120          125
135 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
136           130          135          140
137 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
138 145          150          155          160
139 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
140           165          170          175
141 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
142           180          185          190
143 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
144           195          200          205
145 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
146           210          215          220
147 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
148 225          230          235          240
149 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
150           245          250          255
151 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
152           260          265          270
153 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
154           275          280          285
155 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
156           290          295          300

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157 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
158 305                      310                      315                      320
159 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
160                      325                      330                      335
161 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
162                      340                      345                      350
163 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
164                      355                      360                      365
165 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
166                      370                      375                      380
167 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
168 385                      390                      395                      400
169 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
170                      405                      410                      415
171 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
172                      420                      425                      430
173 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
174                      435                      440                      445
175 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
176                      450                      455                      460
177 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
178 465                      470                      475                      480
179 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
180                      485                      490                      495
181 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
182                      500                      505                      510
183 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
184                      515                      520                      525
185 Arg Leu Ala Arg Gly His Ser Leu
186                      530                      535
188 <210> SEQ ID NO: 3
189 <211> LENGTH: 621
190 <212> TYPE: PRT
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Mutant rep protein: rep78 10 GCG
196 <400> SEQUENCE: 3
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198 1                      5                      10                      15
199 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
200                      20                      25                      30
201 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
202                      35                      40                      45
203 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
204                      50                      55                      60
205 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
206 65                      70                      75                      80
207 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
208                      85                      90                      95

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209	Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
210				100					105					110		
211	Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
212			115					120					125			
213	Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
214		130					135					140				
215	Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
216	145					150				155						160
217	Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
218					165					170					175	
219	Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
220				180					185					190		
221	Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
222			195					200					205			
223	Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
224		210					215					220				
225	Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
226	225					230					235					240
227	Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
228				245						250					255	
229	Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
230				260					265					270		
231	Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
232			275					280						285		
233	Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
234		290					295					300				
235	Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
236	305					310					315					320
237	Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
238				325						330					335	
239	Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
240				340						345					350	
241	Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
242			355					360					365			
243	Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
244		370					375					380				
245	Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
246	385					390					395					400
247	Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
248				405							410				415	
249	Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
250				420					425					430		
251	Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
252			435					440						445		
253	Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
254		450					455					460				
255	Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
256	465					470					475					480
257	Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala

VERIFICATION SUMMARY

DATE: 01/10/2006

PATENT APPLICATION: US/10/022,390A

TIME: 14:30:42

Input Set : E:\912SEQ.002.txt

Output Set: N:\CRF4\01102006\J022390A.raw